

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	563	36.9	602	195	AA037313	zC52103.r1 Soares sen
2	327	21.4	346	73	H876769	yW23922.r1 Homo sapi
3	187	12.2	458	49	HU366909B	Human aorta cDNA 5'-e
4	173	11.3	370	49	HUM345688B	Human aorta cDNA 5'-e
5	114	7.5	303	49	H865591B	Human aorta cDNA 5'-e
6	114	7.5	387	49	HUN366611B	Human aorta cDNA 5'-e
7	56	3.7	157	140	C02463	HUMG0012349, Human G
8	24	1.6	504	5	T7414	yc72a77.r1 Homo sapi
9	23	1.5	344	61	HJ4106	ma762a57.r1 Homo sapi
10	23	1.5	442	5	T71938	ye07cc4.r1 Homo sapi
11	23	1.5	470	2	T60480	yB95033.s1 Homo sapi
12	21	1.4	221	53	R94606	yq39gb0.s1 Homo sapi
13	22	1.4	241	44	H37487	15616 Arabidopsis tha
14	21	1.4	253	129	HSC0BE062	H. sapiens partial cD
15	22	1.4	267	148	W10583	ma3810_r1 Soares mou
16	22	1.4	300	183	HA100384	zn46108.r1 Stratagene
17	22	1.4	301	48	HUN245F10B	Human aorta cDNA 5'-e
18	21	1.4	365	65	T79937	ym60H07.s1 Homo sapi
19	21	1.4	325	112	ATTS3517	A. thaliana transcript
20	21	1.4	325	19	T51964	yb42a03.r1 Homo sapi
21	22	1.4	330	13	RICG037A	Rice cDNA, partial
22	21	1.4	339	88	H65000	yu66d10.0.s1 Homo sapi
23	22	1.4	360	154	C14856	Human fetal brain cDN
24	21	1.4	362	5	T70903	yc49d03.s1 Homo sapi
25	21	1.4	380	187	A8142684	mq64605.r1 Soares 2NB
26	22	1.4	385	180	AA087288	mol1006.r1 Life Tech
27	22	1.4	387	109	HSDR2303	H. sapiens partial cD
28	21	1.4	395	5	T71079	yc66d10.0.s1 Homo sapi
29	22	1.4	406	125	W76826	me73011.r1 Soares mou
30	21	1.4	408	41	R72733	yH53a01.r1 Homo sapi
31	22	1.4	410	6	T74804	yc66d04.r1 Homo sapi
32	21	1.4	447	184	AA011021	ze34a01.s1 Soares ret
33	21	1.4	450	193	NU8886	T9ES273910.r1 Toxop
34	21	1.4	453	193	AA164719	tg50c04.r1 Stratagene
35	22	1.4	453	111	N21157	yx47011.s1 Homo sapi
36	21	1.4	465	193	AA164056	mt670106.r1 Soares mou
37	22	1.4	465	6	T773510.r1 Homo sapi	yd76040.r1 Homo sapi
38	22	1.4	472	57	T42477	5740 Arabidopsis thal
39	21	1.4	472	147	AA037313	mg480101.r1 Soares mou
40	21	1.4	478	172	AA061056	mg480101.r1 Soares mou
41	21	1.4	480	175	W1191	me93111.r1 Soares mou
42	21	1.4	493	55	RIC81559A	Rice cDNA, partial
43	21	1.4	500	94	N38845	yy800d11.s1 Homo sapi
44	22	1.4	796	117	W29026	55C10 Human retina cD
45	21	1.4	798	115	W22001	62G8 Human retina cD









ORIGIN      Query Match      1.5%:      Score 23:      DB 5:      Length 42:

	Best Local Similarity	Local Similarity	Matches	Pred.	NO.	3.63e-05
	31;	conservative	0;	Mismatches	8;	Indels
Db	332	aggacatggaaacaggtttcaggcgttctgtttt	370			
Cp	1022	AGGACATGGTCACTGGTTGATGCCTTATTTGTTT	984			

**ACCESSION** ALPHA-1-MICROGLOBULIN (HUMAN);  
**NID** 9653517  
**KEYWORDS** EST.  
**SOURCE** human clone-78917 library-Stratagene liver (#93724), (kanamycin resistant)  
**ORGANISM** Homo sapiens  
**REFERENCE** vector=plbluescript SK host=S0UR cells (kanamycin resistant)  
**PRIMER** -1ml3 Rsite1=ECORI Rsite2=XbaI Cloned unidirectionally.  
**AUTHORS** primer: Oligo dR. Hepatocyte from normal 49 year old male  
**REFERENCE** caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGACGAG-3'; 3' adaptor sequence: 5'-CTCGAGTTTTTTTTTT-3'.  
**PRIMER** 1 (bases 1 to 470)  
**AUTHORS** Eucaryote; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
**REFERENCE** Holman,M., Hultman,M., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Raskin,L., Rohlfing,T., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R..  
**TITLE** WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)  
**COMMENT**  
**CONTACT** Wilson RK  
**WASHU-MERCK EST PROJECT**  
**WASHINGTON UNIVERSITY SCHOOL OF MEDICINE**  
**4444 FOREST PARK PARKWAY, BOX 8501, ST. LOUIS, MO 63108**  
**TEL:** 314 286 1800  
**FAX:** 314 286 1810  
**EMAIL:** est@wuston.wustl.edu  
**HIGH QUALITY SEQUENCE STOPS:** 374  
**SOURCE:** IMAGE Consortium, LILN  
**THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LILN; CONTACT THE IMAGE CONSORTIUM (INFO@IMAGE.LILN.GOV) FOR FURTHER INFORMATION.**  
**LOCATION** (Qualifiers  
**1.470**  
**/ORGANISM**="Homo sapiens"  
**/CLONE**="78917"  
**/EST**  
**FEATURES**  
**SOURCE**  
**BASE COUNT** 95 a 137 c 125 g 108 t 5 others  
**ORIGIN**  
**RESULT** 12  
**LOCUS** R94906 222 bp mRNA EST  
**DEFINITION** Y939b08.s1 Homo sapiens cDNA clone 198135 3'.  
**ACCESSION** EST  
**NID** 99733636  
**KEYWORDS** EST.  
**SOURCE** human clone-198135 primer-Prromega -21ml3 library-Soares fetal liver spleen LMP1S vector RTP77D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Kpn I Rsite3=Sal I  
**DEFINITION** EST.  
**ACCESSION** R94906  
**NID** 99733636  
**KEYWORDS** EST.  
**SOURCE** human clone-198135 primer-Prromega -21ml3 library-Soares fetal liver spleen LMP1S vector RTP77D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Kpn I Rsite3=Sal I  
**DEFINITION** EST.  
**ACCESSION** R94906  
**NID** 99733636

TITLE	
JOURNAL	
COMMENT	
Contact: Wilson RK	
WashU-Merck EST Project	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: test@watsen.wustl.edu	
High quality sequence stops: 201	
Source: IMAGE Consortium, LBL	
This clone is available royalty-free through LBL ; contact the	
IMAGE Consortium (info@image.llnl.gov) for further information.	
FEATURES	
Source	/clone="398135", /organism="Homo sapiens"
BASE COUNT	31 a 84 c 1 g 77 t 29 others
ORIGIN	<1..>222
	Query Match 1.4%; Score 21; DB 53; Length 222;
LOCUS	Best Local Similarity 60.0%; Prod. No. 1.36e-02;
DEFINITION	Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
ACCESSION	H37487
NID	9906986
KEYWORDS	EST
RESULT	13
SOURCE	H37487 241 bp mRNA EST
DEFINITION	15615 Arabidopsis thaliana cDNA clone 182E10T7.
ACCESSION	H37487
NID	9906986
EST	EST
	thale cress clone-182E10T7 library-Lambda-PR12 strain-var Columbia
vector-Lambda Zip-Lox primer-T7 dye primer Rsite1-Sai Rsite2-Not	
Lambda PR12 is a cDNA library derived from equal quantities of 4	
pools of mRNA. The mRNA source were 1) 7 day germinated etiolated	
seedlings; 2) tissue culture grown roots; 3) day germinated plants half	
with 24 hour light cycle, half on 16 hr light, 8 hour dark.	
rosettes; 4) same plants as 3 but treated tissue (stems, flowers	
and silques. The vector is BRL's lambda Zip-Lox. The cDNA	
inserts were directionally cloned with Sal-Not arms using oligo dT	
primed cDNA.	
ORGANISM	Arabidopsis thaliana
	Euphorbiaceae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
REFERENCE	Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 241)
	Newman,T., de Brujin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,J., Ohlridge,J., Raikhel,N., Somerville,S., Thomsen,M., Retzel,E. and Somerville,C.
TITLE	Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL	Plant Physiol. 106, 1241-1255 (1994)	source	1..253
COMMENT	Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-0168 Email: 22313tcn@ibm.cl.msu.edu.		/organism="Homo sapiens" /isolate="muscular atrophy patient" /dev_stage="3 months old" /tissue_type="total brain" /clone_id="182E107" /strain="var columbia"
FEATURES	Location/Qualifiers		/sex="Female"
SOURCE	1..241		
BASE COUNT	72 a 72 c 50 g 70 t 8 others	BASE COUNT	76 a 57 c 49 g 70 t 1 others
ORIGIN		ORIGIN	
RESULT	14	Query Match	1..4%; Score 21; DB 129; Length 253;
LOCUS	HSCEB062	st Local Similarity	78.4%; Pred. No. 1..36e-02;
DEFINITION	253 bp RNA	Matches	0; Mismatches 8;
ACCESSION	239433	Indels	0; Gaps 0;
NID	9560441	DEFINITION	m38f10 r1 soares mouse p3Mf19 5
KEYWORDS	partial cDNA sequence; transcribed sequence fragment.	ACCESSION	Mus musculus mRNA clone 313003 5'
SOURCE	human.	REFERENCE	W10583
ORGANISM	Homo sapiens	AUTHORS	91284900
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Buteraria; Primates; Catarhini; Hominidae; Homo.	TITLE	ACACAGCTCACAGAGACAGACTTCAGCTGAG 810
AUTHORS	1 (bases 1 to 253)	JOURNAL	
TITLE	Direct Submission	COMMENT	
JOURNAL	Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France and Genelique Moleculaire et Biologie du Developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France. E-mail: genexpress@genethon.fr	CONTACT	Maria M/Mouse EST Project
REFERENCE	2 (bases 1 to 253)	WASHU-HMM	WashU-HMM Mouse EST Project
AUTHORS	Genexpress.	WASHU	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TITLE	The Genexpress cDNA program	FOREST	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
JOURNAL	Unpublished	PHONE	Tel: 314 286 1800
REFERENCE	3 (bases 1 to 253)	FAX	Fax: 314 286 1810
JTHORS	Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Desigenes,M.D., Duprat,S., Houlgate,R., Juneau,M.N., Lam,B., Lorenzo,F., Mitchell,R., Marjorie-Sanson,R., Pietu,G., Pouliot,Y., Sebastiano-Kabakchis,C. and Tessier,A.	EMAIL	Email: mouseest@atson.wustl.edu
IMAGE	molecular integration of the analysis of the human genome	IMAGE	This clone is available royalty-free through LILN: contact the IMAGE Consortium (infoimage.lnl.gov) for further information.
FEATURES	source	PIRIM	Primer: Full length read
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)	SEQ PRIMER	Seq primer: EPrimer
MEDLINE	95277534	LOCATION/QUALIFIERS	Location/Qualifiers
COMMENT	Clone library from B. Soares, Psychiatry Dept. Columbia University USA;	1..267	
IMAGE	molecular integration of the analysis of the human genome	/organism="Mus musculus"	
FEATURES	source	/note="vector: pT7T3D (Pharmacia) with a modified	
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)	polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA	
REFERENCE	Sequencing_method: single read, full automatic;	was primed with Not I - oligo(dT) primer [5'-	
PRIMER	(-21)M13 universal;	TCTTACCATCGAGCTGGACGGCCGATTTTTTTTTTTTTTTT 3']'	
CDNA	CDNA sequence complementary to mRNA (3' end)	double stranded cDNA was size selected, ligated to Eco RI	
STRETCH	Cloning method: total mRNA was oligo(dT) primed and directionally	adapters (Pharmacia), digested with Not I and cloned into	
REMOVED	cloned 5' -> 3' into the HindIII -> NotI sites of the lambda Ba	the Not I and Eco RI sites of a modified pT7T3 vector	
NORMALIZATION	vector;	(Pharmacia). Library went through one round of	
METHOD	Sequencing method: single read, full automatic;	normalization to a Cot = 5. Library constructed by Bento	
GENEXPRESS	Primer: (-21)M13 universal;	Soares and M. Fatima. Bento. RNA was kindly provided by	
LIBRARY	Genexpress library id: C;	Dr. Minoru KO (Wayne State University). "clone_id="313003"	
ID	Genexpress_sequence_idt: alc-0be06;	/clone_id="Soares mouse p3Mf19 5"	
GENEXPRESS	No significant homology found with :	/dev_stage="19.5 dpc total fetus"	
FEATURES	genbank release 81 swissprot release 28.	/lab_stage="DH10B (ampicillin resistant)"	
BASE COUNT	78 a 70 c 61 g 58 t	mRNA	<1..>257
ORIGIN		BASE COUNT	

